



003300-883.ST25

10/019566  
10 Rec'd PCT/PTC 21 MAR 2003

SEQUENCE LISTING

<110> Leif, Leif

<120> RECOMBINANT ADENOVIRUS

<130> 003300-883

<140> US 10/019,566

<141> 2002-03-28

<150> SE 9902601-5

<151> 1999-07-06

<150> US 60/143,632

<151> 1999-07-14

<150> PCT/SE00/01390

<151> 2000-06-30

<160> 16

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 36

<212> PRT

<213> Homo sapiens

<300>

<301> Hoppe HJ, Barlow PN, Reid KBM

<302> A parallel three stranded a-helical bundle at the nucleation site of collagen triple-helix formation

<303> FEBS Letters

<304> 344

<306> 191-195

<307> 1994

<400> 1

Pro Asp Val Ala Ser Leu Arg Gln Gln Val Glu Asp Leu Gln Gly Gln

1

5

10

15

Val Gln His Leu Gln Ala Ala Phe Ser Gln Tyr Lys Lys Val Glu Leu

20

25

30

Phe Pro Asn Gly

35

<210> 2

<211> 31

<212> PRT

<213> Homo sapiens

<300>

<301> Harbury PB, Zhang T, Kim PS, Albert T

<302> A switch between two-, three-, and four-stranded coiled coils in GCN4 leucine zipper mutants

<303> Science

<304> 262

<306> 1401-1407  
 <307> 1993-11-26

<400> 2  
 Met Lys Gln Ile Gly Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr  
   1                  5                  10                  15  
 His Ile Glu Asn Gly Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu  
           20                  25                  30

<210> 3  
 <211> 6  
 <212> PRT  
 <213> Pseudomonas aeruginosa

<300>  
 <301> Brinkmann U, Buchner J, Pastan I  
 <302> Independent domain folding of Pseudomonas exotoxin and single  
       chain immunotoxins: Influence of interdomain connections  
 <303> Proc. Natl. Acad. Sci. US  
 <304> 89  
 <306> 3075-3079  
 <307> 1992

<400> 3  
 Ala Ser Gly Gly Pro Glu  
   1                  5

<210> 4  
 <211> 7  
 <212> PRT  
 <213> Homo sapiens

<300>  
 <301> Brinkmann U, Buchner J, Pastan I  
 <302> Independent domain folding of Pseudomonas exotoxin and single  
       chain immunotoxins: Influence of interdomain connections  
 <303> Proc. Natl. Acad. Sci. US  
 <304> 89  
 <306> 3075-3079  
 <307> 1992

<400> 4  
 Ala Ser Glu Gly Asn Ser Asp  
   1                  5

<210> 5  
 <211> 8  
 <212> PRT  
 <213> Mus musculus

<300>  
 <301> Brinkmann U, Buchner J, Pastan I  
 <302> Independent domain folding of Pseudomonas exotoxin and single  
       chain immunotoxins: Influence of interdomain connections  
 <303> Proc. Natl. Acad. Sci. US  
 <304> 89

<306> 3075-3079  
 <307> 1992

<400> 5  
 Ala Ser Thr Pro Glu Pro Asp Pro  
 1 5

<210> 6  
 <211> 13  
 <212> PRT  
 <213> Staphylococcus aureus

<400> 6  
 Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ser Asp  
 1 5 10

<210> 7  
 <211> 11  
 <212> PRT  
 <213> Homo sapiens

<300>  
 <301> Dengl JL, Wensel TG, Morrison SL, Streyer L, Herzenberg LA,  
 and Oi T  
 <302> Segmental flexibility and complement fixation of genetically  
 engineered chimeric human, rabbit and mouse antibodies  
 <303> EMBO Journal  
 <304> 7  
 <306> 1989  
 <307> 1988

<400> 7  
 Thr Pro Leu Gly Asp Thr Thr His Thr Ser Gly  
 1 5 10

<210> 8  
 <211> 11  
 <212> PRT  
 <213> Adenovirus type 5

<300>  
 <301> Stouten PFW, Sander C, Ruigrok WH, Cusack S  
 <302> New triple-helical model for the shaft of the adenovirus fibre  
 <303> Journal of molecular biology  
 <304> 226  
 <306> 1073-1084  
 <307> 1992

<400> 8  
 Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
 1 5 10

<210> 9  
 <211> 8  
 <212> PRT

<213> Simian virus 40

<300>

<301> Fisher-Fantuzzi L and Vesco C

<302> Cell-Dependent Efficiency of Reiterated Nuclear Signals in a  
Mutant Simian Virus 40 Oncoprotein Targeted to the Nucleus

<303> Molecular Cell Biology

<304> 8

<306> 5495-5503

<307> 1992

<400> 9

Asp Pro Lys Lys Lys Arg Lys Val

1

5

<210> 10

<211> 116

<212> PRT

<213> Homo sapiens

<400> 10

Gln Lys Val Thr Gln Ala Gln Thr Glu Ile Ser Val Val Glu Lys Glu

1

5

10

15

Asp Val Thr Leu Asp Cys Val Tyr Glu Thr Arg Asp Thr Thr Tyr Tyr

20

25

30

Leu Phe Trp Tyr Lys Gln Pro Pro Ser Gly Glu Leu Val Phe Leu Ile

35

40

45

Arg Arg Asn Ser Phe Asp Glu Gln Asn Glu Ile Ser Gly Arg Tyr Ser

50

55

60

Trp Asn Phe Gln Lys Ser Thr Ser Ser Phe Asn Phe Thr Ile Thr Ala

65

70

75

80

Ser Gln Val Val Asp Ser Ala Val Tyr Phe Cys Ala Leu Gly Gly Val

85

90

95

Asn Asn Asn Ala Gly Asn Met Leu Thr Phe Gly Gly Gly Thr Arg Leu

100

105

110

Met Val Lys Pro

115

<210> 11

<211> 133

<212> PRT

<213> Homo sapiens

<400> 11

Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro

1

5

10

15

Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu

20

25

30

Ala Thr Gly Phe Phe Pro Asp His Val Glu Lys Ser Trp Trp Val Asn

35

40

45

Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys

50

55

60

Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu

65

70

75

80

Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys

85

90

95

Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp

[illegible]

```
<210> 13
<211> 53
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Sequence replacing the fiber gene sequence which was deleted between the NdeI restriction site in the fiber tail and the MunI site which begins at base 38 after the stop codon in the fiber. The sequence restores the NdeI and MunI sites and the wild type genome sequence between the fiber stop codon and the MunI site. In addition the added sequence contains an XhoI site allowing for the ligation of recombinant fibers.

<400> 13  
tatgcactcg agtaaagaat cgtttgtgtt atgtttcaac gtgtttatTTt ttc 53

```
<210> 14
<211> 1746
<212> DNA
<213> Human adenovirus type 5
```

```
<220>
<221> CDS
<222> (1)...(1746)
<223> 1-129 Fiber tail
      130-1200 Fiber shaft
```

## 1201-1746 Fiber knob

&lt;400&gt; 14

atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca	48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro	
1 5 10 15	
tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc	96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro	
20 25 30	
ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct	144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser	
35 40 45	
ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc	192
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu	
50 55 60	
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc	240
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser	
65 70 75 80	
caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac	288
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn	
85 90 95	
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta	336
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu	
100 105 110	
act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc	384
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr	
115 120 125	
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att	432
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile	
130 135 140	
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa	480
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln	
145 150 155 160	
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act	528
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr	
165 170 175	
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg	576
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu	
180 185 190	
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg	624
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly	
195 200 205	
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act	672
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr	
210 215 220	

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act	720
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr	
225 230 235 240	
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca	768
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala	
245 250 255	
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt	816
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val	
260 265 270	
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag	864
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln	
275 280 285	
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac	912
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn	
290 295 300	
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag	960
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu	
305 310 315 320	
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata	1008
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile	
325 330 335	
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca	1056
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro	
340 345 350	
aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat	1104
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp	
355 360 365	
tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac	1152
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp	
370 375 380	
agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act	1200
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr	
385 390 395 400	
ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag	1248
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu	
405 410 415	
aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata	1296
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile	
420 425 430	
ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata	1344
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile	
435 440 445	
tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat	1392
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn	
450 455 460	

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 1440  
 Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe  
 465 470 475 480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac ggt gtt gga 1488  
 Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Gly Val Gly  
 485 490 495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 1536  
 Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala  
 500 505 510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 1584  
 Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys  
 515 520 525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 1632  
 Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp  
 530 535 540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 1680  
 Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly  
 545 550 555 560

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca 1728  
 His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser  
 565 570 575

tac att gcc caa gaa taa 1746  
 Tyr Ile Ala Gln Glu \*  
 580

<210> 15  
 <211> 121  
 <212> PRT  
 <213> Mus musculus

<400> 15  
 Asp Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys Leu Gly Gly  
 1 5 10 15  
 Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr  
 20 25 30  
 Tyr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Leu Val  
 35 40 45  
 Ala Ala Ile Asn Ser Asp Gly Gly Ile Thr Tyr Tyr Leu Asp Thr Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu Phe Tyr Cys  
 85 90 95  
 Ala Arg His Arg Ser Gly Tyr Phe Ser Met Asp Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Ser Val Thr Val Ser Ser Gly Ser  
 115 120

<210> 16



<211> 116  
 <212> PRT  
 <213> Mus musculus

<400> 16  
 Asp Ile Val Met Thr Gln Ser Gln Arg Phe Met Ser Thr Thr Val Gly  
 1 5 10 15  
 Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Val Ser Ala  
 20 25 30  
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile  
 35 40 45  
 Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Met Gln Ser  
 65 70 75 80  
 Glu Asp Leu Ala Asp Phe Phe Cys Gln Gln Tyr Ser Asn Tyr Pro Trp  
 85 90 95  
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala  
 100 105 110  
 Pro Thr Val Ser  
 115